Exhibit 2:

Alignment of SEQ ID NO:2 with C-type Lectin Domains

rat MBP	K F **F** V T N H E R M P **F** S K **V** K A L **C** S E L R G T **V** A I **P** R N
	β1 α1
human E-selectin	W S **Y** N T S T E A M T **Y** D E **A** S A Y **C** Q Q R Y T H **L** V A **I** Q N
rat ML	S C **Y** W F S Q S G K P **W** P E **A** D K Y **C** Q L E N S N **L** V V **V** N S
SEQ ID NO:2	V I **Y** F H D T SRR L N **F** E E **A** K E A **C** R R D G G Q **L** V S **I** E S
	44 75
rat MBP	A E **E** N K **A** **I** Q E V A K T S A **F** **L** **G** **I** T **D** E V T E G Q **F**
	α2 β2
human E-selectin	K E **E** I E **Y** **L** N S I L S YSP S Y Y **W** **I** **G** **I** R **K** V N N V **W**
rat ML	L A **E** Q N **F** **L** Q T H M G S V V T **W** **I** **G** **L** T **D** Q N G P **W**
SEQ ID NO:2	E D **E** Q K **L** **I** E K F I ENLLP SDGDF **W** **I** **G** **L**RRR**E**EK QSNSTACQDL**Y**
	76 117
rat MBP	M **Y** V T **G** G R **L** T Y S **N** **W** K K D **E** **P** **N** **D** H G S G **E** **D** **C**
	β3 **
human E-selectin	V **W** V G T **Q** K P **L** T E E A K **N** **W** A P G **E** **P** **N** **N** R Q K D **E** **D** **C**
rat ML	R **W** V D **G** T D **Y** E K G F T **H** **W** A P K **Q** **P** **D** **N**WYGHGLGGG**E** **D** **C**
SEQ ID NO:2	A **W** T D **G** S **I** S Q F R **N** **W** Y V D **E** **P** **S** **C** G S **E** **V** **C**
	118 142
rat MBP	**V** T **I** V D N **G** L **W** **N** **D** I S **C** Q A S H T A **V** C **E** F P
	β4 β5** ** β6
human E-selectin	**V** E **I** Y IKR EKD V **G** M **W** **N** **D** E R **C** S K K K L A **L** C **Y** T A
rat ML	**A** H **F** T S D **G** R **W** **N** **D** D V **C** Q R P Y R W **V** C **E** M K
SEQ ID NO:2	**V** V **M** Y HQPSAPAGIG**G**PYMFQ**W** **N** **D** D R **C** N M K N N F **I** C **K** Y S
	143 179

This Exhibit is based on Figure 1 of Exhibit 1: Bajorath, J., 1996, "A molecular model of the carbohydrate recognition domain of a rat macrophage lectin and analysis of its binding site", *Journal of Molecular Graphics* **14**: 297-301.

MBP: mannose-binding protein; ML: macrophage lectin.

Residues in boldface correspond to boxed residues in Figure 1 of Exhibit 1 (Bajorath, 1996, *Journal of Molecular Graphics* **14**: 297-301), and represent residues thought to be determinants of the C-type lectin fold.

Horizontal shaded bars indicate the structurally conserved regions in MBP and E-selectin.

Regions labeled α1-α2 and β1-β6 are major secondary structure elements in E-selectin.

Double asterisks indicate the functional calcium-binding site of MBP.

The residue numbering shown below each set of sequences is that of SEQ ID NO:2.